AMENDMENTS TO THE SPECIFICATION

Applicant hereby directs entry of the Substitute Sequence Listing submitted herewith into the Specification

Please replace the paragraph that spans from page 16 to page 18 with the following paragraph:

The term "similarity" as used herein includes exact identity between compared sequences at the nucleotide or amino acid levels. Where there is non-identity at the nucleotide level "similarity" includes differences between sequences which result in different amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. Where there is non-identity at the amino acid level, "similarity" includes amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. The percentage similarity may be greater than 45% such as at least 50% or at least 55% or at least 60% or at least 65% or at least 70% or at least 75% or at least 80% or at least 85% or at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or higher. To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences may be aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions can then be compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i. e. % identity = # of identical positions/total # of overlapping positions x 100). Preferably, the two sequences are the same length. The determination of percent identity or homology between two sequences can be accomplished using a mathematical algorithm. A suitable, mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87: 2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215 : 403-410.

BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See the world wide web at ncbi.nlm.nih.gov ~~http://www.ncbi.nlm.nih.gov~~. Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted. Yet another example of a suitable algorithm is one such Gap which considers all possible alignment and gap positions and creates an alignment with the largest number of matches bases and the fewest gaps. Gap uses the alignment method of Needleman and Wunsch. Gap reads a scoring matrix that contains values for ever possible GCG symbol match. GAP is available on ANGIS (Australian National Genomic Information Service) on the internet at mell.angis.org.au ~~at website http://mell.angis.org.au~~.

Please replace the First full paragraph on page 60 with the following paragraph:

Rabbit polyclonal peptide antisera against the DEC-205 CP domain and the DCL-1 CP were produced by immunizing New Zealand White rabbits with diphtheria toxoid- conjugated synthetic peptide CEDEIMLPSFHD (SEQ ID NO: 33) and CGEENEYPYQFD (SEQ ID NO: 34) (Minotopes, Clayton, VIC, Australia), respectively, using a conventional schedule with Freund adjuvant at the Herston Medical Research Institute (Herston, QLD, Australia). To assess the titer of the antibodies against CP peptides, an ELISA plate was coated with streptavidin (Sigma) and biotinylated peptides for DEC-205 CP (biotin-SGSGEDEIMLPSFHD, SEQ ID NO: 35) and

DCL-1 CP (biotin-SGSGEENEYPYQFD, SEQ ID NO: 36) captured. The plate was blocked with 1% (w/v) sodium caseinate (Sigma) in PBS and 0.1% (w/v) Tween20 (PBS/Tw), and incubated with serially diluted antisera. After washing the plate with PBS/Tw, bound antibody was detected with HRP-sheep anti rabbit IgG and o-phenylenediamine hydrochloride, and quantitated with 492 nm using an ELISA reader. There was no cross-reactivity detected between these two rabbit CP antibodies at the dilutions used in the experiments described (data not shown).

Please replace Table 3 on page 77 with the following table:

Table 3. The DNA sequences of oligonucleotides primers used in this study

Primer	Sequence (5'>3')	SEQ ID NO
062	GACCATGGAGCGGACATGATA	~~<400>~~23
063	GGCTCTACCATCTGGGTTTGT	~~<400>~~24
078	CCGCCATGTCGCGCGGCCT	~~<400>~~25
085	ACCAAATCAGTCCGCCCATGAGAA	~~<400>~~26
086	ATCATGTCCGCTCCATGGTCAGTA	~~<400>~~27
088	TATTCAGAAGTTAAAAGCAGA	~~<400>~~28
090	CCAAAAGGCCGTACTCCAAAA	~~<400>~~29
092	GGAGGAAAACTGAATGACGCA	~~<400>~~30
094	GAAAACGGTTGTGAAGATAAT	~~<400>~~31